

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2002, 09:58:11 ; Search time 1598.42 Seconds

(without alignments)
16317.389 Million cell updates/sec

Title: US-09-603-124B-1

Sequence: 1 gcaagtaacgctccacggt.....gacgtatgaacaaagcag 1581

Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 1472140 segs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenBank: 1: gb.pa:*
2: gb.hlg:*
3: gb.in:*
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5: gb.ov:*
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35: em.hlg.tod:*
36: em.hlg.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	1581	100.0	349980	6	AX127150	AX127150 Sequence
2	1458	92.2	1458	6	AX122446	AX122446 Sequence
3	1122	71.0	2291	1	AB015023	AB015023 Corynebacter
4	1050	66.4	1458	6	E28467	E28467 Novel muc
5	951	60.2	4622	1	BLA242646	BLA242646 Corynebact
6	236	14.9	4116	1	AB003132	AB003132 Corynebact
7	236	14.9	5546	1	BLF257	BLF257 Corynebacter
8	63	4.0	1116	6	AX122447	AX122447 Sequence
9	21	1.3	1073	8	AF022730	AF022730 Oryza sat
C 10	21	1.3	6843	2	AC019805	AC019805 Drosophila
C 11	21	1.3	85875	9	AC010010	AC010010 Drosophila
C 12	21	1.3	126039	2	AC012665	AC012665 Homo sapi
C 13	21	1.3	137569	2	AC084093	AC084093 Homo sapi
C 14	21	1.3	163027	2	AC028246	AC028246 Homo sapi
C 15	21	1.3	174822	2	AC013275	AC013275 Homo sapi
C 16	21	1.3	175590	2	AF0307159	AF0307159 Homo sapi
C 17	21	1.3	181848	2	AC090199	AC090199 Homo sapi
C 18	21	1.3	310120	3	AE003468	AE003468 Drosophila
C 19	20	1.3	234	8	TA0131670	TA0131670 Triticum
C 20	20	1.3	1263	6	AX122173	AX122173 Sequence
C 21	20	1.3	1374	6	AX122688	AX122688 Sequence
C 22	20	1.3	1556	6	AX064415	AX064415 Sequence
C 23	20	1.3	52650	2	AC010026	AC010026 Drosophila
C 24	20	1.3	157541	2	AX127149	AX127149 Sequence
C 25	20	1.3	349980	6	AX127151	AX127151 Sequence
C 26	20	1.3	349980	6	AX127151	AX127151 Sequence
C 27	19	1.2	11994	1	AE005031	AE005031 Halobacter
C 28	19	1.2	15000	8	AF169016	AF169016 Aspergillus
C 29	19	1.2	32274	1	SCC8A	SCC8A Streptococcus
C 30	19	1.2	56917	1	AME16952	AME16952 Amycolatops
C 31	19	1.2	67480	2	AF279874	AF279874 Homo sapi
C 32	19	1.2	85217	8	AT017713	AT017713 Human DNA
C 33	19	1.2	104770	9	HSJ245M18	HSJ245M18 Homo sapi
C 34	19	1.2	109612	9	AL512503	AL512503 Human DNA
C 35	19	1.2	114856	9	HS0808E14	HS0808E14 Homo sapi
C 36	19	1.2	116501	2	AC008053	AC008053 Homo sapi
C 37	19	1.2	119060	2	AC023390	AC023390 Homo sapi
C 38	19	1.2	119456	2	AC084789	AC084789 Homo sapi
C 39	19	1.2	131047	2	AC002421	AC002421 Homo sapi
C 40	19	1.2	139232	2	AL353762	AL353762 Homo sapi
C 41	19	1.2	144727	9	HSJ646P11	HSJ646P11 Homo sapi
C 42	19	1.2	145382	2	AC073223	AC073223 Homo sapi
C 43	19	1.2	148260	2	AL596222	AL596222 Homo sapi
C 44	19	1.2	148882	2	AC018381	AC018381 Homo sapi
C 45	19	1.2	150436	2	AC024119	AC024119 Homo sapi

ALIGNMENTS

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VERSION	AX127150.1	GI:14041138						
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ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
FEATURES								
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 Matches 1581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 121 ttctgacaagaatattgatctgtccgcgctcacctcatcgattggcgagcgagat 180
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 Db 182603 TTCTGCACAAAGATATTGATCTGTCCGGGTCCACCTCATGGAATTGGCGAGCCGAA 182544
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 Db 182543 GTCTGCGGTTGCGGAACTCTCTGTCCCGCGGTAAAGACAGTCACTGTTCCGATGCCAA 182484
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 Db 182483 AGATTCCCGACCTTCTCTCACTCCGCGCGGTGGAGCCACCATCGAGTGGAGACAC 182424
 QY 301 tgcggaacaccttgaactcttcgagaaactccacacgctgtgttaactcttttgcgcg 360
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 Db 182303 TCGCTCCGATCTTGTGGGGAATTCCTGGAAGCTCCACCGAGCTTTGATGGCGGATAC 182244
 QY 481 ccaagtaagacactccacacactctatgtctgtgtatgacatgacgaagcgagatga 540
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 QY 541 tccaagcttgcctatcgcgacagctcaacaagctgtgacacatgacacatgagac 600
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 QY 781 tgtgtgcctgaacagatcctcaacgaagcagctgtgggagagagctgtctgtccgaaggat 840
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 Db 181943 TGTGTGCTTAAAGATCCCTCAAGCGAGAGCTGGGAGAGAGTGTGTCGCCGAAGGAT 181884
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 DEFINITION Sequence 2362 from Patent EP1108790.
 ACCESSION AX122446
 VERSION AX122446.1 GI:14039691
 KEYWORDS
 SOURCE Corynebacterium glutamicum.
 ORGANISM Corynebacterium glutamicum.
 Bacteria: Firmicutes; Actinobacteria; Actinobacteriales;
 Actinomycetales; Corynebacteriineae; Corynebacteriaceae;
 Corynebacterium.
 1 (bases 1 to 1458)
 REFERENCES
 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
 Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and, Ozaki, A.
 Novel polynucleotides
 Patent: EP 1108790-A 2362 20-JUN-2001;
 KYOWA HAKKO KOGYO CO., LTD. (JP)
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 /db_xref="taxon:1718"
 BASE COUNT 318 a 420 c 400 g 320 t
 ORIGIN

Query Match 92.2%; Score 1458; DB 6; Length 1458;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 161 ggtatctggcggagacgggaatgtctggcggttgcgggaatctctgctggcggcggtgaaga 220
 Db 61 GGTATCTGGCGGAGACCGGAATGTCTGGCGGTTCGCCGAATCTGCTTGCCTCCGGGTAAGACA 120
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 581 accaatcgac 640
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 Db 781 CACCCTGAGGTCCAGGAGGT 840
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 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
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 1 (bases 1 to 2291)

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 AUTHORS
 TITLE
 JOURNAL
 FEATURES
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ORIGIN

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QY 112 agacttgatttcacaaatatatctgcgcgcgtccacactatcgtattcgcg 171
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DB 105 acacttgatttcacaaatatatctgcgcgcgtccacactatcgtattcgcg 164

QY 172 agccggaatgtctcggttgcgcgaatcctgtctgcgcgcgttaagacagtcagtttc 231
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QY 352 ttltgcgcgcacttcgcgaagaacacccggaacttgcgtgcagtggaagaagcattcc 411
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QY 472 cgcgggtacccacgtaagaactccacacactatctgttgcgtatgcagtcagc 531
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DB 645 ctacaagccaatgttgcagtggttcacacatgttgcgaagcagacacacttgacttttaa 704

QY 712 aaccctgaagcactactccaagtgctgcagatcttcgagcagcatcaccgccgaacg 771

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DB 705  AACCCTGAAGCCTACTTCTCAAGTCTTGAGACATTTGCGAGACGATACCCCAAGC 764
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DB 765  caaactgtgtgtgtgcctgaagaacatccacacgagcagcgtgaggaaggtctgtcgc 824
QY 832  caaaggtatcaagaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 891
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DB 825  caaaggtatcaagaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 884
QY 892  tccagcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 951
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DB 885  tccagcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 944
QY 952  caaactgtatgaacaggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1011
    |||||
DB 945  caaactgtatgaacaggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1004
QY 1012 caaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1071
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DB 1005 caaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1064
QY 1072 tgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1131
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DB 1065 tgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1124
QY 1132 gggcggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1191
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DB 1125 gggcggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1184
QY 1192 aactgcagtgctgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1251
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DB 1185 aactgcagtgctgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1244
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DB 1245 cgtgcgttccacacacatltatcaccagcaccatagaatccacaaagaggtctgcgcg 1304
QY 1312 ggcagtgctgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1371
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DB 1305 ggcagtgctgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1364
QY 1372 ggtgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1431
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DB 1365 ggtgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1424
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DB 1425 acccaattctctgcagtgccacgaagcagcagcagcagcagcagcagcagcagcagcagcag 1484
QY 1492 gcttaccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1551
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DB 1485 gcttaccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1544
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DB 1545 aaacaattagagcgtgaagtgaagaagcag 1574

RESULT 4
E28467 1458 bp DNA PAT 07-FEB-2001
LOCUS E28467
DEFINITION Novel murc gene.
ACCESSION E28467.1 GI:13018359
VERSION JP 1999196876-A/1.
KEYWORDS
SOURCE
ORGANISM Corynebacterium glutamicum.
Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
Actinomycetales; Corynebacteriaceae; Corynebacterium.
REFERENCE 1 (bases 1 to 1458)

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JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4622)
 AUTHORS Gil, J. A.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-1999) Gil J. A., Microbiology, University of Leon,
 Campus de Vegazana s/n, 24071 Leon, SPAIN

102A

FEATURES
 Location/Qualifiers

1. 4622

/organism="Corynebacterium glutamicum"

/strain="ATCC 13869"

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/evidence="experimental"

/product="MurD protein"

/protein_id="CAB6322.1"

/db_xref="GI:6723456"

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336. 1808

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 AGTRATINIDGOEVSIIQIPDHWLGAALAGLVGVDVLDKLEGLSPFSVGR
 RRFEEFGAIEGKFNCAIYDDVAHHPTETVLAALRYAKGKRVIAVAPPHLY
 SRTEFOKEFPAELSLADAIVLEIGAREOPVDSSEIITDAMTIPVYERNFSAY
 PRRIEAGIPNDIVLTWAGSVYMLAPETLIDLONN"

BASE COUNT 989 a 1254 c 1317 g 1062 t
 ORIGIN

Query Match 60.2%; Score 951; DB 1; Length 4622;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1201; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 gcaagtaacgcccctcagcagtgatctgacagccttgatctgacacatcaatgccaac 60
 DB 3047 GCAGTAAACCCCTCCACGCTGATTCACACATGATTCCTCACTATCAATAGCCACAC 3106
 QY 61 aactaaagcagcagcctcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
 DB 3107 AACTAAACGACGACCTCCACGCTGATTCACACATGATTCCTCACTATCAATAGCCACAC 3166
 QY 121 ttcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 DB 3167 TTCGACACAGATATGATCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGAT 3226
 QY 181 gtcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
 DB 3227 GTCGCGGCTGCGGACGATCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGAT 3286
 QY 241 agatcccgacccctctcaccaccccgccgctgagcagcagcagcagcagcagcagcagcagc 300
 DB 3287 AGATTCGCCGACCTTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGAT 3346
 QY 301 tgcggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
 DB 3347 TCGGGAACCTTGAATCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGAT 3406
 QY 361 catcccgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
 DB 3407 CATCCCGACGACCTTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGAT 3466
 QY 421 tgcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
 DB 3467 TCGCTCGACATCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGAT 3526
 QY 481 ccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
 DB 3527 CCACGGAACGACCTTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGAT 3586
 QY 541 tccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
 DB 3587 TCCAAGCTTCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGATGAT 3646
 QY 601 tgcggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
 DB 3647 TGGGAGGCTTCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGATGAT 3706
 QY 661 aaatgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
 DB 3707 AAATGTGAGCTTCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGAT 3766
 QY 721 agcctactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
 DB 3767 AGCCTACTCTCTCTCCGCGTCCACTCTATGATGATGATGATGATGATGATGATGATGAT 3826
 QY 781 tgcggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840
 DB 3827 TGTGTGCTGAGAGATCTCTACGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3886

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Db	3887	CAAGACTGTGTGGTATACGTAACCCGTAAGCAAGTACAGCAACCCGTGAGGTTCCAGGAT	3946
QY	901	gagtcacatctgtgattcccaagtgtgtgcagaagagcaaccgagccacatacaatcga	960
Db	3947	GAGTCACGCTGTGGATTGCCAAATGTTGTCAGAAAGGCAACCGCCACCATCAATCAATCGA	4006
QY	961	tggacaagaagatattcgtatcttccttaaatcccttcgtgatcatatgtrtactaaagctgc	1020
Db	4007	TGGACAGGAAGATCTGTGATTTCTTAATCCCTCGTGATCAATCATGTACTCAACGGTGC	4066
QY	1021	agccgacccgtgagccgagatacttgatgagtgaggagctgacaaactgtttgaagcctt	1080
Db	4067	AGCCGCCCTGCTGGCCGGAATCCTGTTGGGTGGGAGCTGTGAATACCTTTGTAAGCTT	4126
QY	1081	gtcggattctccggcgtgtgcagccgcgtttgagttccacggtgctatcgagggcggca	1140
Db	4127	GTCGGATTCTCCGCGCTGTGCAGCCGCTTTGAGTTCACGGTGTGAGAGGCGGCA	4186
QY	1141	attcaatgagcgtctatattatgatattatgacgacacacacacaaaggaagtaactgagt	1200
Db	4187	ATTTAATGGCGCTGCTATTATGATGATTACGACACACCAACCAAGAACTGACGT	4246
QY	1201	gtccag 1206	
Db	4247	GCTCA 4252	
RESULT	6		
LOCUS	AB003132	4116 bp DNA	04-AUG-1997
DEFINITION		Corynebacterium glutamicum gene for MurC, FtsQ, complete cds.	
ACCESSION	AB003132		
VERSION	AB003132.1	GI:2308989	
KEYWORDS	FtsZ; FtsQ; MurC.		
SOURCE		Corynebacterium glutamicum	
ORGANISM		Corynebacterium glutamicum	
REFERENCE		Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;	
AUTHORS		Corynebacterium.	
TITLE		1 (bases 1 to 4116)	
JOURNAL		Kobayashi, M.	
REFERENCE		Direct Submission	
		Submitted (15-APR-1997) to the DDBJ/EMBL/GenBank databases. Miki	
		Kobayashi, Mitsubishi Chemical Corp., Tsukuba Research Center; Ami	
		(E-mail: 3709292@cc.m.kagaku.co.jp, Tel: 0298-87-1011,	
		Fax: 0298-87-3259)	
REFERENCE		2 (sites)	
AUTHORS		Kobayashi, M., Asai, Y., Hatakeyama, K., Kijima, N., Wachi, M., Nagai, K.	
TITLE		and Yukuwa, H.	
JOURNAL		Cloning, sequencing, and characterization of the ftsZ gene from	
MEDLINE		Corynebacterium bacteria.	
FEATURES		biochem. Biophys. Res. Commun. 236 (2):383-388 (1997)	
source		97382442	
gene		Location/Qualifiers	
gene		1. 4116	
gene		/organism="Corynebacterium glutamicum"	
gene		/db_xref="taxon:1718"	
gene		1. 273	
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gene		/codon_start=1	
gene		/transl_table=11	
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gene		/protein_id="BAA21665.1"	
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gene		/translation="EF0KFEAALSLADAAVLYEYGARQPDVGSSELTIDANTIF	
gene		VYVERPESAVPERIAEINGRNDIVLMGASVTMLAPEILDQANN"	
gene		301. 969	
gene		/gene="ftsQ"	

[illegible]

Db 238 GCTCCAGAAATCTGGATCAGCTGCAGAAACAAATAGGAGTGAAGTGAACAGGACAG 293

RESULT 7
BLPFSZ 5546 bp DNA BCT 19-JAN-2000
LOCUS Brevibacterium lactofermentum murec(partial), ftsQ, ftsZ genes and
DEFINITION ORS5, ORF6 DNA.
ACCESSION Y08864
VERSION Y08864.2 GI:6723445
KEYWORDS cell division protein; divb gene; division initiation protein; ftsQ
gene; ftsZ gene; murec gene; putative YAK 1 protein; putative YP75
protein; UDP-N-acetylmuramate-alanine ligase.
SOURCE Corynebacterium glutamicum.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
REFERENCE 1 (bases 1 to 5546)
AUTHORS Homrubi, M.P., Fernandez, F.J. and Gil, J.A.
TITLE Identification, characterization, and chromosomal organization of
the ftsZ gene from Brevibacterium lactofermentum
J. Gen. Genet. 259 (1), 97-104 (1998)
JOURNAL MoL. Gen. Genet. 259 (1), 97-104 (1998)
REFERENCE 2 (bases 1 to 5546)
AUTHORS Gil, J.A.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1996) J.A. Gil, Universidad de Leon,
Microbiologia, Campus de Vegazana S/N, 24071 Leon, SPAIN
REMARK Revised by [3]
AUTHORS 3 (bases 1 to 5546)
TITLE G11, J.A.
JOURNAL Direct Submission
COMMENT Submitted (24-MAY-1999) J.A. Gil, Universidad de Leon,
Microbiologia, Campus de Vegazana S/N, 24071 Leon, SPAIN
FEATURES
Location/Qualifiers
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/translation="KEFAALSLADAIVLEIYGAREPVDGVSSEIITDMATIPVY
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292..960
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GSLNGVSGADNRNVVATROALINSPLEATPMDCATVILSPAGSDIVFMSNA
SMVRESPEVDVNLIFGTLIDNLDGDEVRTVIATGPDARASAEENRAGIPAPAE
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SGANVEPEAMARVDEAKPLGSIARTTKGTGDIIRAGLLQMSLIGQIMDSDPCT
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BASE COUNT 1317 a 1479 c 1520 g 1230 t
ORIGIN

Query Match 14.9% Score 236; DB 1; Length 5546;
Best Local Similarity 100.0%; Pred. No. 5; 5e-119;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1346 gagattcagcagcgcgcaacaaccggtggaatgctgctcctggaaatcaacgat 1405
DB 49 GAGATTTCAGCGAGCGCGCAACACCGGTGATGCTGCTCCGGAATCATCACCAT 108
QY 1406 gcgaatgacattcgaatgctgcaaacctattcctcagtcagtcacgaacgat 1465
DB 109 GCGATGACCATTCATGCTGTGACGACCATTAATTCCTGCAATCCCAAGCATTC 168
QY 1466 gaatcgcagacctaatacgtgctgcacatggatggatgacggttcgctgacatgct 1525
DB 169 GAAATCGACGACCTAATGCTGCTCACCATGGGTCCAGATTCCCTGACCATGCTT 228
QY 1526 gctccagaatcctgcatcagctgcaaaacattagagctgaatgacagcgac 1581

Db 229 GCTCCAGAATCTCTGATCAGCTGCAAAACATTAGGACGTAAGTGAACAAGGCG 284

RESULT	8				
AX122447					
LOCUS	AX122447	1116 bp	DNA	PAT	11-MAY-2001
DEFINITION	Sequence 2363 from Patent EP1108790.				
ACCESSION	AX122447				
VERSION	AX122447.1	GI:14039694			
KEYWORDS					
SOURCE	Corynebacterium glutamicum.				
ORGANISM	Corynebacterium glutamicum.				

FEATURES	RYOMA HAKKO KOGYO CO., LTD. (JP)
SOURCE	Location/Qualifiers
	1. 1116
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	/db_xref="taxon:1718"
BASE COUNT	234 a 317 c 319 g 246 t
ORIGIN	

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Query Match          4.0%; Score 63; DB 6; Length 1116;
Best Local Similarity 100.0%; Pred. No. 4.8e-23;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 ggcggaaagcctccacggatgatgttcgacgaacatgatgtctgcaactatcatatgaccaaac 60
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Db 1054 GCGGGAACGCTCCACGCGTATGTCAGACATGATGTCGCAACTATCATATGACCAACAC 1113

OY 61 aac 63
      |||
Db 1114 AAC 1116

RESULT 9
LOCUS AF022730 1073 bp. mRNA PLN 30-OCT-1997
DEFINITION Oryza sativa, glyceraldehyde-3-phosphate dehydrogenase subunit
(GAPDH), partial cds.
ACCESSION AF022730
VERSION AF022730
KEYWORDS AF022730.1 GI:2570494
ORGANISM Oryza sativa.
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzoae; Oryza.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Lee,M.C., Kim,C.S. and Eun,M.Y.
TITLE Isolation and characterization of glyceraldehyde-3-phosphate
dehydrogenase from rice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1073)
AUTHORS Lee,M.C., Kim,C.S. and Eun,M.Y.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1997) CytoGenetics, National Institute of
Agricultural Science and Technology, RDA, Sedun-Dong, Suwon
441-707, Korea
FEATURES
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	/dev stage="immature (milky stage)"
gene	/clone="KCDM2189"
CDS	1..>1073 /gene="GAPDH" 45..>1073 /gene="GAPDH" /codon_start=1 /product="glyceraldehyde-3-phosphate dehydrogenase subunit" /protein_id="AA88213.1" /db_xref="GI:2570495" translation="MASPCSPPPCHSRGGGLSDPSGLRSESLIPRLPANSIDPNMPVSRFTAVGTONGGARAPAPRAKIKLVANIGFRRPLRIQWHRGRDDSPINITGVGEKQKSRIRYKNSTLTICPDADIVPGVNPISVCETIKVSRPRNSNIPMGELGISLLEGGTSPHNANGSGTIOMAKKVIILPKPGDIPYYVGVAADQSPDPISLNSCTNCNLAAPRYVLIDKQGTLTKGNTHTSHSYGDQRVDGSHRLPRARAALINTVFYSTGAARVALVPLNAGKLNGIALTNFTFWSVYDVLYQVSCKTLAEVNAQAROSAAANEIWAASREER
BASE COUNT	196 a 380 c 335 g 162 t
ORIGIN	

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Query Match 1.3%; Score 21; DB 2; length 6843;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 actccgcgcgtggagaccac 282
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Db 5976 acttcgcgccttggagaccac 5956

RESULT 11
AC010010

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LOCUS AC010010 85875 bp DNA HTG 18-FEB-2000
 DEFINITION Drosophila melanogaster clone RPCI98-13f6, *** SEQUENCING IN
 ACCESSION AC010010
 VERSION AC010010.3 GI:6996694
 KEYWORDS HTG: HTGS_PHASE1.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Phlebotomidae; Drosophilidae; Drosophila.
 1 (bases 1 to 85875)
 Munz, D.M., Adams, C., Bailey, M., Barberia, J., Blankenburg, K.,
 Bodota, B., Bouck, J., Bowler, S., Brooks, A., Buhay, C., Bunc, C.,
 Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
 David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Bashid, N.,
 Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
 Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
 Guevara, M., Harris, K., Hernandez, J., Hodgson, A., Hogue, M.,
 Holloway, C., Hosak, R., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
 Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
 Licherage, O., Liu, J., Liu, W., Logan, O., Lozano, R.J., Lu, J.,
 Morris, S., Nash, S., Nelson, A., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
 Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L.,
 Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
 Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, R., Sugrue, R.,
 Taber, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wabnitz, M.,
 Wellington, S., Weinstein, G., Weinstein, I.R., Williamson, A.,
 Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
 Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 85875)
 Morley, R.C.
 Direct Submission
 Submitted (11-SEP-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Feb 18, 2000 this sequence version replaced gi:5881484.
 ***** Genome Center *****
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ***** Project Information *****
 Center project name: RPCI98-13f6
 Center clone name: RPCI98-13f6
 ***** Summary Statistics *****
 Sequencing vector: M13; L08821
 Chemistry: Dye-terminator Big Dye; 68% of reads
 Assembly program: Phrap; version 0.980611
 Consensus quality: 41466 bases at least Q40
 Consensus quality: 57245 bases at least Q30
 Consensus quality: 64735 bases at least Q20
 Estimated insert size: 75108; sum-of-coverage estimation
 Quality coverage: 0.8x in Q20 bases; sum-of-coverage estimation
 ***** NOTE: This is a 'working draft' sequence. It currently
 * consists of 53 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1256: contig of 1256 bp in length
 * 1257 1276: gap of unknown length
 * 1277 2355: contig of 1079 bp in length
 * 2356 2375: gap of unknown length
 * 2376 3452: contig of 1077 bp in length
 * 3453 3472: gap of unknown length

3473 4275: contig of 803 bp in length
 4276 4295: gap of unknown length
 4296 5562: contig of 1267 bp in length
 5563 5582: gap of unknown length
 5583 6777: contig of 1195 bp in length
 6778 6797: gap of unknown length
 6798 8061: contig of 1264 bp in length
 8062 8081: gap of unknown length
 8082 9053: contig of 972 bp in length
 9054 9074: gap of unknown length
 9074 9934: contig of 861 bp in length
 9935 9955: gap of unknown length
 9955 10765: contig of 812 bp in length
 10766 10786: gap of unknown length
 10787 11616: contig of 830 bp in length
 11617 11636: gap of unknown length
 11637 12464: contig of 828 bp in length
 12465 12484: gap of unknown length
 12485 13645: contig of 1161 bp in length
 13646 13665: gap of unknown length
 13666 14489: contig of 824 bp in length
 14490 14510: gap of unknown length
 14510 15861: contig of 1332 bp in length
 15862 15881: gap of unknown length
 15882 15921: contig of 1040 bp in length
 15922 15941: gap of unknown length
 15942 16465: contig of 1524 bp in length
 16466 18485: gap of unknown length
 18486 19317: contig of 831 bp in length
 19317 19337: gap of unknown length
 19337 20903: contig of 1567 bp in length
 20904 20923: gap of unknown length
 20924 22150: contig of 1227 bp in length
 22151 22170: gap of unknown length
 22171 23295: contig of 1125 bp in length
 23296 23315: gap of unknown length
 23316 24311: contig of 995 bp in length
 24311 26237: gap of unknown length
 26237 26238: contig of 1887 bp in length
 26238 27816: gap of unknown length
 27816 27835: contig of 1578 bp in length
 27835 28794: gap of unknown length
 28794 28814: contig of 959 bp in length
 28815 30095: gap of unknown length
 30096 30115: contig of 1281 bp in length
 30116 31085: gap of unknown length
 31086 31105: contig of 970 bp in length
 31105 32390: gap of unknown length
 32390 32410: contig of 1285 bp in length
 32410 32425: gap of unknown length
 32425 34245: gap of unknown length
 34246 34265: contig of 1835 bp in length
 34266 35631: gap of unknown length
 35632 35651: contig of 1366 bp in length
 35652 37059: gap of unknown length
 37060 37079: contig of 1408 bp in length
 37080 38607: gap of unknown length
 38607 38627: contig of 1528 bp in length
 38628 40420: gap of unknown length
 40420 40440: gap of 1793 bp in length
 40441 41701: contig of 1261 bp in length
 41702 41721: gap of unknown length
 41722 43339: contig of 1598 bp in length
 43340 43359: gap of unknown length
 43360 45717: contig of 2378 bp in length
 45717 45737: gap of unknown length
 45738 47273: contig of 1536 bp in length
 47274 47293: gap of unknown length
 47294 48892: contig of 1599 bp in length
 48893 48912: gap of unknown length
 48913 50344: contig of 1432 bp in length
 50345 50364: gap of unknown length
 50365 52143: contig of 1779 bp in length

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* 52144 52163: gap of unknown length
* 52164 54492: contig of 2329 bp in length
* 54493 54512: gap of unknown length
* 54513 56276: contig of 1764 bp in length
* 56277 56296: gap of unknown length
* 56297 57684: contig of 1368 bp in length
* 57685 59691: contig of 2007 bp in length
* 59692 59711: gap of unknown length
* 59712 63581: contig of 3870 bp in length
* 63582 65422: contig of 1821 bp in length
* 65423 65443: gap of unknown length
* 65443 67456: contig of 2014 bp in length
* 67457 67476: gap of unknown length
* 67477 69545: contig of 2069 bp in length
* 69546 69565: gap of unknown length
* 69566 72562: contig of 2997 bp in length
* 72563 72582: gap of unknown length
* 72583 75310: contig of 2728 bp in length
* 75311 75330: gap of unknown length
* 75331 77972: contig of 2642 bp in length
* 77973 77992: gap of unknown length
* 77993 82474: contig of 4482 bp in length
* 82475 82495: gap of unknown length
* 82495 85875: contig of 3381 bp in length.

FEATURES
  source
    1. 85875
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone="RP109-13P6"

BASE COUNT  23385 a 18706 c 18751 g 23920 t 1113 others
ORIGIN
  Query Match      1.3% Score 21; DB 2; Length 85875;
  Best Local Similarity 100.0%; Pred. No. 6; 2;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 attccgcgcgtggagccac 282
Db 37850 ACTCGCGCGGTGGAGCCAC 37870

RESULT 12
AC012665/c 126039 bp DNA PRI 03-JUL-2001
LOCUS Homo sapiens clone RP11-19E11, complete sequence.
DEFINITION AC012665
ACCESSION AC012665
VERSION AC012665.8 GI:14589661
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 126039)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 126039)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 126039)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jul 3, 2001 this sequence version replaced gi:13794251.

```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUSGC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project information
Center project name: H.NH0019E11
-----

FEATURES
  source
    1. 126039
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="RP11-19E11"

BASE COUNT  33691 a 29032 c 28371 g 34945 t
ORIGIN
  Query Match      1.3% Score 21; DB 9; Length 126039;
  Best Local Similarity 100.0%; Pred. No. 6;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1537 cctggatcagctgcaaacaa 1557
Db 115904 CCTGGATCAGCTGCAAAACAA 115884

RESULT 13
AC084093/c 137569 bp DNA HTG 09-MAY-2001
LOCUS Homo sapiens chromosome 8 clone CTD-2277K12 map 8, WORKING DRAFT
DEFINITION AC084093
ACCESSION AC084093
VERSION AC084093.2 GI:13123904
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FOLDTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 137569)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone CTD-2277K12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 137569)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bedalov,F., Boguslavsky,L.,
Bouckgalter,B., Brown,A., Burkett,G., Campiano,A., Castle,A.,
Choapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeRellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heathford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Larocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Maconald,P., Margulis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPeeters,R., Meldrum,J., Meneus,L., Mihova,T., Mlengue,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Oliver,T.W., Oliver,J., Peterson,K.,
Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Ribback,M., Riley,R.,
Rougny,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Tirrell,A., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 26, 2001 this sequence version replaced gi:10799458.
All repeats were identified using RepeatMasker:
Smt,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu

```

Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L11391
 Center clone name: 2277_K12
 Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 136529 bases at least Q40
 Consensus quality: 137130 bases at least Q30
 Consensus quality: 137294 bases at least Q20
 Insert size: 139000; agarose-fp
 Quality coverage: 7.8 in Q20 bases; agarose-fp
 Quality coverage: 7.9 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 37849: contig of 37849 bp in length
 * 37850 37949: gap of 100 bp
 * 37950 82422: contig of 44473 bp in length
 * 82423 82522: gap of 100 bp
 * 82523 137569: contig of 55047 bp in length.
 Location/Qualifiers
 1.137569
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="CTD-2277K12"
 /clone_lib="CIRD Human BAC"
 1. 37849
 /note="assembly-fragment"
 misc_feature 37950..82422
 /note="assembly-fragment"
 misc_feature 82523..137569
 /note="assembly-fragment"
 BASE COUNT 42095 a 26887 c 26629 g 41757 t 201 others
 ORIGIN

Query Match 1.3%; Score 21; DB 2; Length 137569;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 863 gctgacgcctacagcacac 883
 ||||||||||||||||
 Db 33227 GCTGACGCCGTACAGCACAC 33207

RESULT 14
 AC022846
 LOCUS
 DEFINITION Homo sapiens chromosome 8 clone RP11-253N21 map 8, WORKING DRAFT
 SEQUENCE, 6 unordered pieces.
 AC022846
 AC022846.3 GI:13123397
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 163027)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 8, clone RP11-253N21
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 163027)

AUTHORS
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A., Choehel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearrellano,K., Dewar,K., Domino,M., Doyle,M., Fensholt,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Gardina,S., Grant,G., Hages,B., Heatford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kain,L., Karatas,A., Klein,J., Lander,E., Lenock,J., Levine,R., Liu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N., McEwan,P., McGuck,A., McKernan,K., McNetters,R., Meldrum,J., Menus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rotman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Rhoman,N., Stojanovic,N., Subramaniam,A., Talmes,J., Tesfaye,S., Theodore,J., Titrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,W.

TITLE
 JOURNAL
 COMMENT
 Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 25, 2001 this sequence version replaced gi:1139770.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www.seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

Project Information
 Center project name: L6163
 Center clone name: 253.N.21

Summary Statistics
 Sequencing vector: M13; M7815; 3% of reads
 Sequencing vector: Plasmid; n/a; 61% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 160669 bases at least Q40
 Consensus quality: 161671 bases at least Q30
 Consensus quality: 162136 bases at least Q20
 Insert size: 157000; agarose-fp
 Insert size: 162527; sum-of-coverage
 Quality coverage: 13.6 in Q20 bases; agarose-fp
 Quality coverage: 13.1 in Q20.

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 23967: contig of 23967 bp in length
 * 23968 24067: gap of 100 bp
 * 24068 25128: contig of 1061 bp in length
 * 25129 25228: gap of 100 bp
 * 25229 34037: contig of 8809 bp in length
 * 34038 34137: gap of 100 bp
 * 34138 56813: contig of 22666 bp in length
 * 56814 56913: gap of 100 bp
 * 56914 92224: contig of 35311 bp in length
 * 92225 92324: gap of 100 bp
 * 92325 163027: contig of 70703 bp in length.
 Location/Qualifiers
 1.163027
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="RP11-253N21"
 /clone_lib="RC1-11 Human Male BAC"
 1. 23967
 /note="assembly-fragment"

misc_feature
 misc_feature
 misc_feature

```

misc_feature      clone_end:SP6
                  vector_side:left
misc_feature      24068..25128
                  /note="assembly_fragment"
misc_feature      25229..34037
                  /note="assembly_fragment"
misc_feature      34138..56813
                  /note="assembly_fragment"
misc_feature      56914..92224
                  /note="assembly_fragment"
misc_feature      92325..163027
                  /note="assembly_fragment"
                  clone_end:T7
                  vector_side:right
BASE COUNT      48042 a 32608 c 32206 g 49671 t 500 others
ORIGIN
Query Match      1.3% Score 21: DB 2: Length 163027:
Best Local Similarity 100.0%: Pred. No. 5.9;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ox 863 gctgacgcgtacagcacac 883
Db 90055 GCTGACCCGCTACAGCACAC 90075
|||||
AC013275      174822 bp DNA PRI 09-AUG-2001
DEFINITION      Homo sapiens BAC clone RP11-464C8 from 2, complete sequence.
ACCESSION      AC013275
VERSION      AC013275.8 GI:15144471
KEYWORDS      HTG.
SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 174822)
                Sulston, J.E. and Waterston, R.
                Toward a complete human genome sequence
                Genome research 8 (11), 1097-1108 (1998)
REFERENCE      2 (bases 1 to 174822)
                Sun, H., Haakenson, W. and Connors, J.
                The sequence of Homo sapiens BAC clone RP11-464C8
                Unpublished
REFERENCE      3 (bases 1 to 174822)
                Waterston, R.H.
                Direct Submission
                Submitted (05-NOV-1999) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
                4 (bases 1 to 174822)
                Waterston, R.
                Direct Submission
                Submitted (09-AUG-2001) Department of Genetics, Washington
                University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                On Aug 9, 2001 this sequence version replaced g1:13270787.
                Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: saplens@wustl.wustl.edu
                Summary Statistics
                Center project name: H_NH0464C08

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., paired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Cataneese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pictet de Jong and coworkers at the Roswell Park Cancer Institute (<http://daccpac.med.buffalo.edu>)
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-393J17; the clone sequenced to the right is AC016076. Actual start of this clone is at base position 1 of RP11-464C8; actual end is at base position 174822 of RP11-464C8.

The region between 76913 to 76922 is covered only by a single m13 subclone. Digest information confirms the assembly.

```

FEATURES
    source
        1..174822
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="2"
        /map="2"
        /clone="RP11-464C8"
        /clone_id="RP11-11"
        /rpt_family="MER2_type"
        1305..1548
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        1864..1954
        /rpt_family="MIR"
        1955..2254
        /rpt_family="Alu"
        2255..2334
        /rpt_family="MIR"
        3496..4429
        /note="similar to EST AL589988 (NID:913396825)"
        5380..5666
        /rpt_family="Alu"
        6188..6501
        /rpt_family="Alu"
        6975..6998
        /rpt_family="(TTTG)n"
        8647..8809
        /rpt_family="Alu"
        8823..8884
        /rpt_family="MER2_type"
        9261..9396
        /rpt_family="MER1_type"
        9397..9711
        /rpt_family="Alu"
        9712..9758
        /rpt_family="MER1_type"
        10174..10321
        /rpt_family="Alu"
        10322..10366
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        10367..10453
        /rpt_family="Alu"
        10467..10527
        repeat_region

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10604. .10930
/rpt_family="ERV1"
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10931. .10942
/rpt_family="Alu"
repeat_region /rpt_family="Alu"
10943. .10974
/rpt_family="(G)n"
repeat_region /rpt_family="Alu"
10975. .11271
/rpt_family="Alu"
repeat_region /rpt_family="ERV1"
11272. .11629
/rpt_family="ERV1"
repeat_region /rpt_family="ERV1"
11629. .11925
/rpt_family="ERV1"
repeat_region /rpt_family="ERV1"
12011. .12316
/rpt_family="Alu"
repeat_region /rpt_family="Alu"
12389. .12763
/rpt_family="ERV1"
repeat_region /rpt_family="ERV1"
12764. .12798
/rpt_family="MaLR"
repeat_region /rpt_family="MaLR"
12799. .13097
/rpt_family="Alu"
repeat_region /rpt_family="Alu"
13098. .13493
/rpt_family="MaLR"
repeat_region /rpt_family="MaLR"
13494. .13832
/rpt_family="MaLR"
repeat_region /rpt_family="MaLR"
13833. .14250
/rpt_family="ERV1"
repeat_region /rpt_family="ERV1"
14251. .15502
/rpt_family="MaLR"
repeat_region /rpt_family="MaLR"
15505. .15912
/rpt_family="MaLR"
repeat_region /rpt_family="MaLR"
15968. .16092
/rpt_family="ERV1"
repeat_region /rpt_family="ERV1"
16797. .17059
/rpt_family="MERL_type"
repeat_region /rpt_family="MERL_type"
18122. .18307
/rpt_family="MERL_type"
repeat_region /rpt_family="ERV1"
18309. .18885
/rpt_family="ERV1"
repeat_region /rpt_family="Alu"
18953. .19126
/rpt_family="Alu"
repeat_region /rpt_family="Alu"
19909. .20210
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24684. .25493
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Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 6112 CCTGATCAGTCGCAAAACAA 6132

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Search completed: February 15, 2002, 10:47:55
Job time: 2984 sec